Report

	dataset_5.dat	dataset_6.dat
# contigs (>= 0 bp)	3	4
# contigs (>= 1000 bp)	3	2
Total length (>= 0 bp)	6710	5870
Total length (>= 1000 bp)	6710	5460
# contigs	3	2
Largest contig	3980	3360
Total length	6710	5460
Reference length	10000	10000
GC (%)	51.28	52.44
Reference GC (%)	52.07	52.07
N50	3980	3360
NG50	1610	2100
N75	1610	2100
L50	1	1
LG50	2	2
L75	2	2
# misassemblies	1	2
# misassembled contigs	1	1
Misassembled contigs length	3980	3360
# local misassemblies	0	0
# unaligned contigs	0 + 0 part	0 + 0 part
Unaligned length	0	0
Genome fraction (%)	67.100	54.600
Duplication ratio	1.000	1.000
# N's per 100 kbp	0.00	0.00
# mismatches per 100 kbp	0.00	0.00
# indels per 100 kbp	0.00	0.00
# genes	5 + 4 part	1 + 6 part
# operons	1 + 1 part	0 + 2 part
# predicted genes (unique)	8	7
# predicted genes (>= 0 bp)	8	7
# predicted genes (>= 300 bp)	7	6
# predicted genes (>= 1500 bp)	0	1
# predicted genes (>= 3000 bp)	0	0
Largest alignment	2030	2100
NA50	1950	1471
NGA50	1610	700
NA75	1610	1189
LA50	2	2
LGA50	3	4
LA75	3	3

All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).
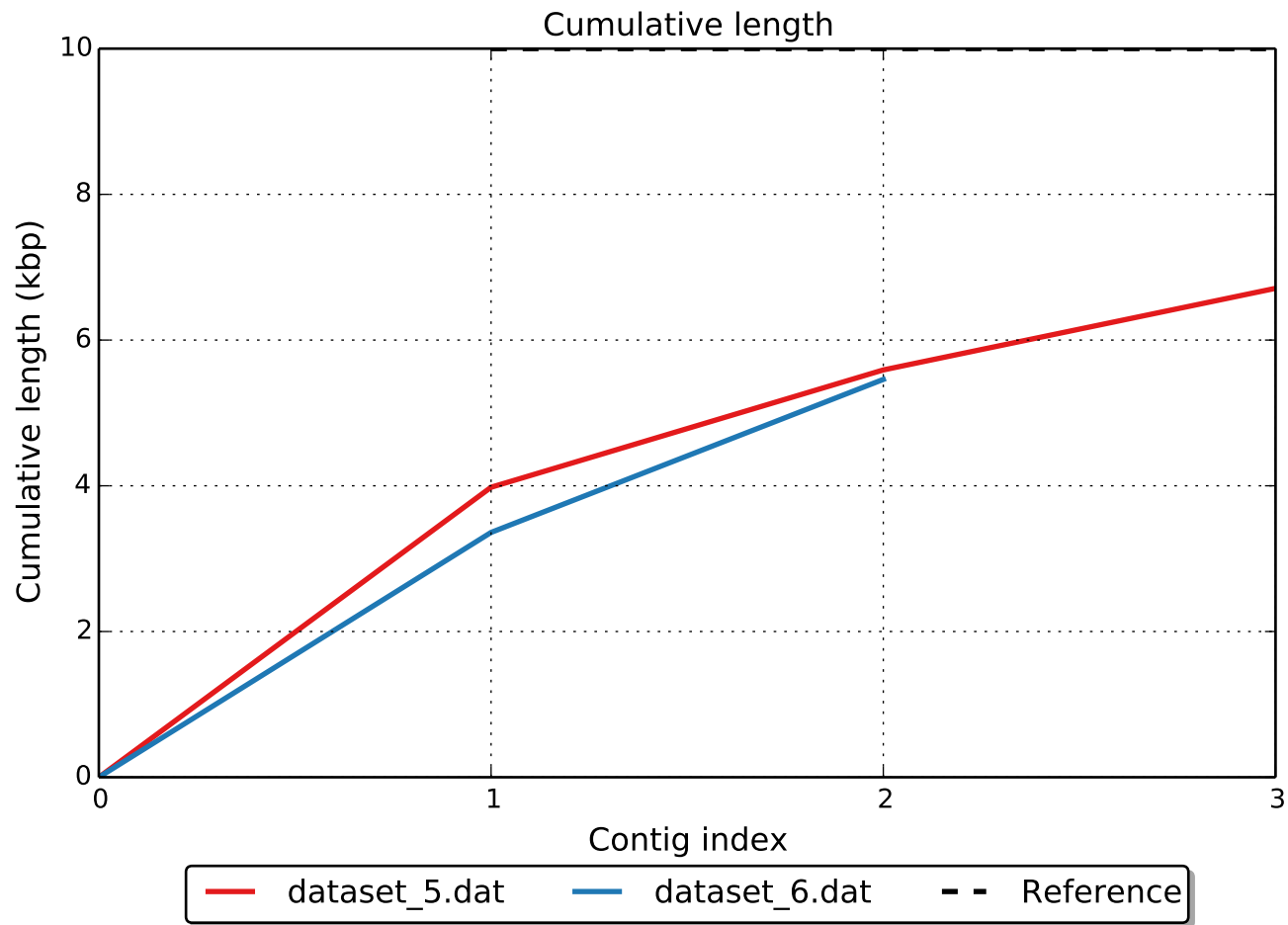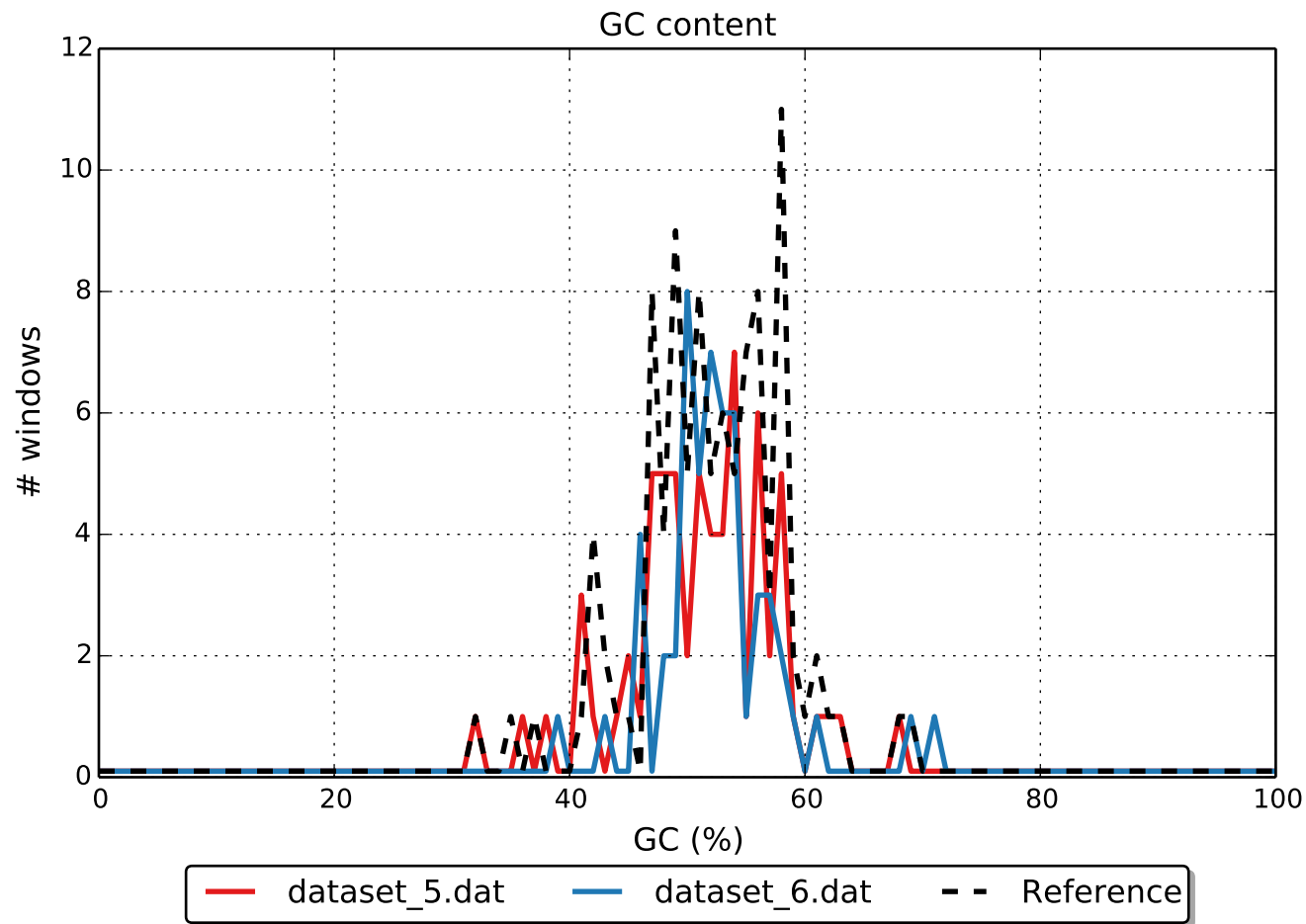
Misassemblies report

	dataset_5.dat	dataset_6.dat
# misassemblies	1	2
# relocations	1	2
# translocations	0	0
# inversions	0	0
# misassembled contigs	1	1
Misassembled contigs length	3980	3360
# local misassemblies	0	0
# mismatches	0	0
# indels	0	0
# short indels	0	0
# long indels	0	0
Indels length	0	0

All statistics are based on contigs of size >= 500 bp, unless otherwise noted
(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Unaligned report
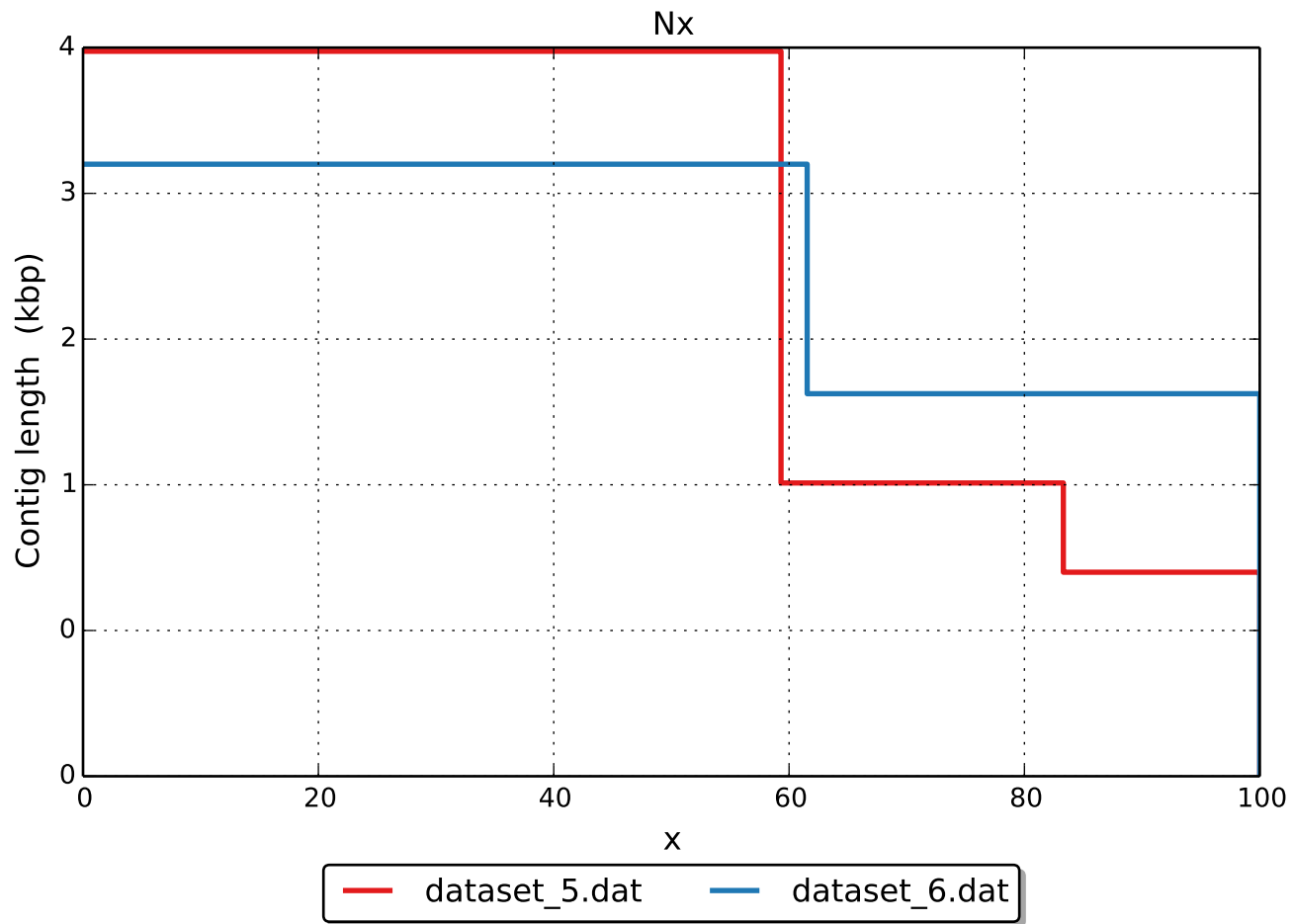
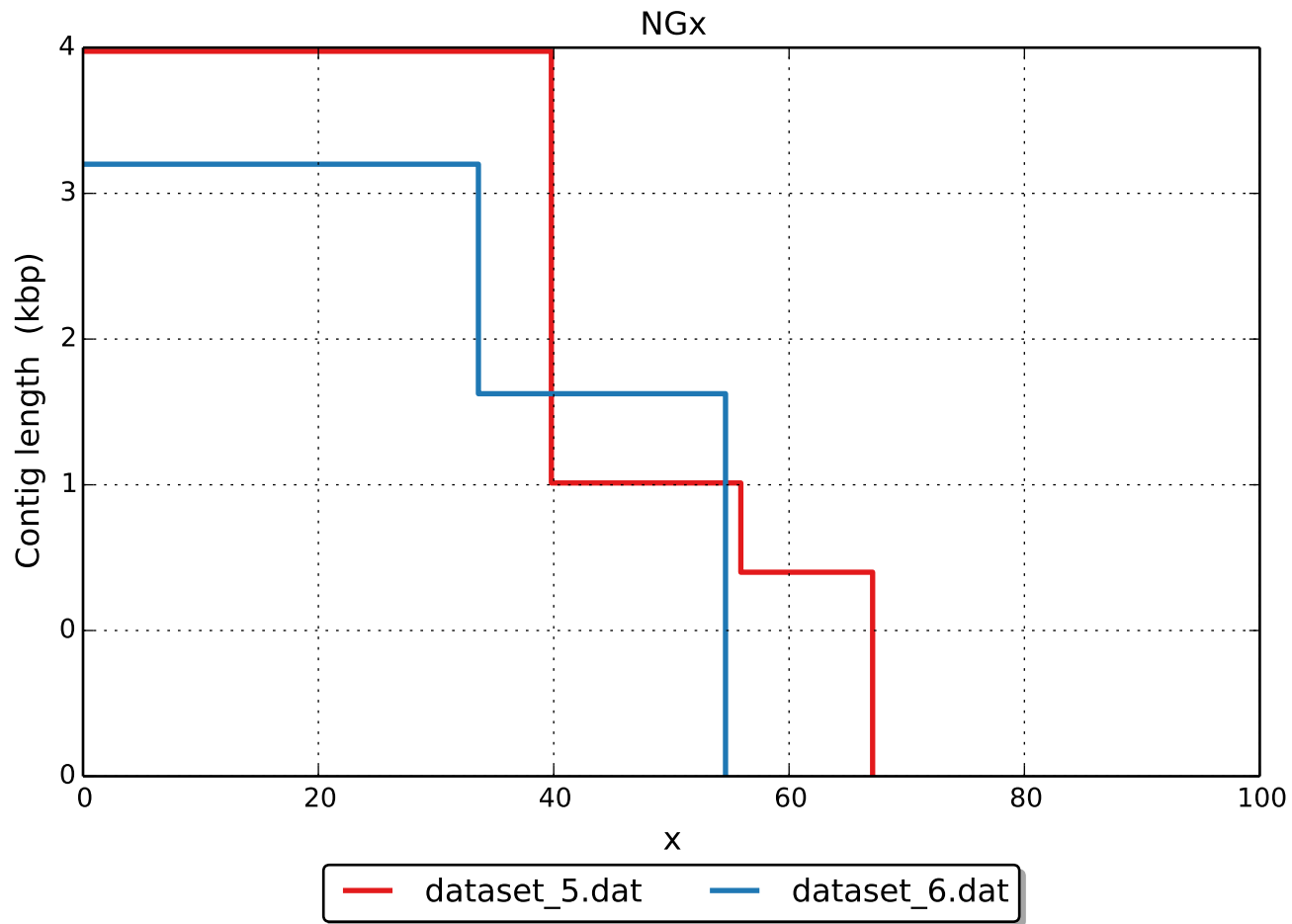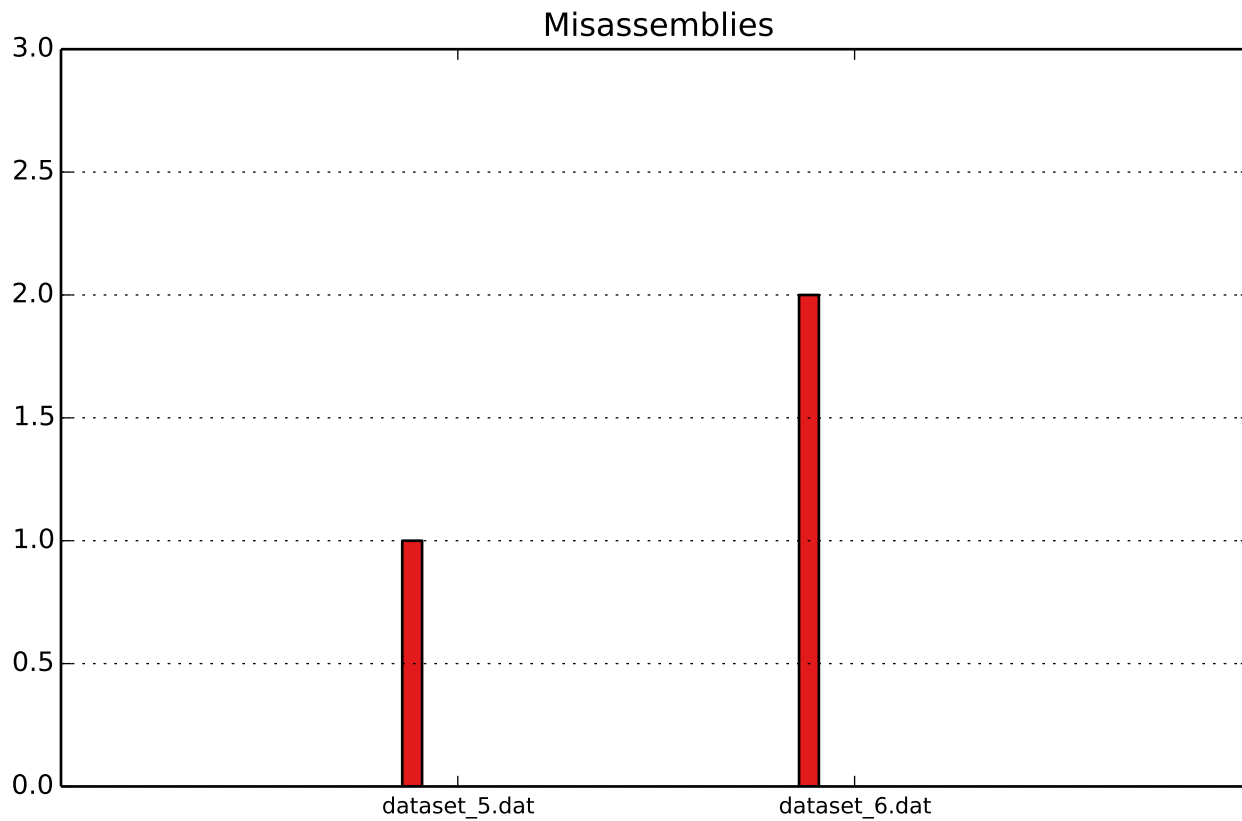|	dataset_5.dat	dataset_6.dat
# fully unaligned contigs	0	0
Fully unaligned length	0	0
# partially unaligned contigs	0	0
# with misassembly	0	0
# both parts are significant	0	0
Partially unaligned length	0	0
# N's	0	0

All statistics are based on contigs of size >= 500 bp, unless otherwise noted
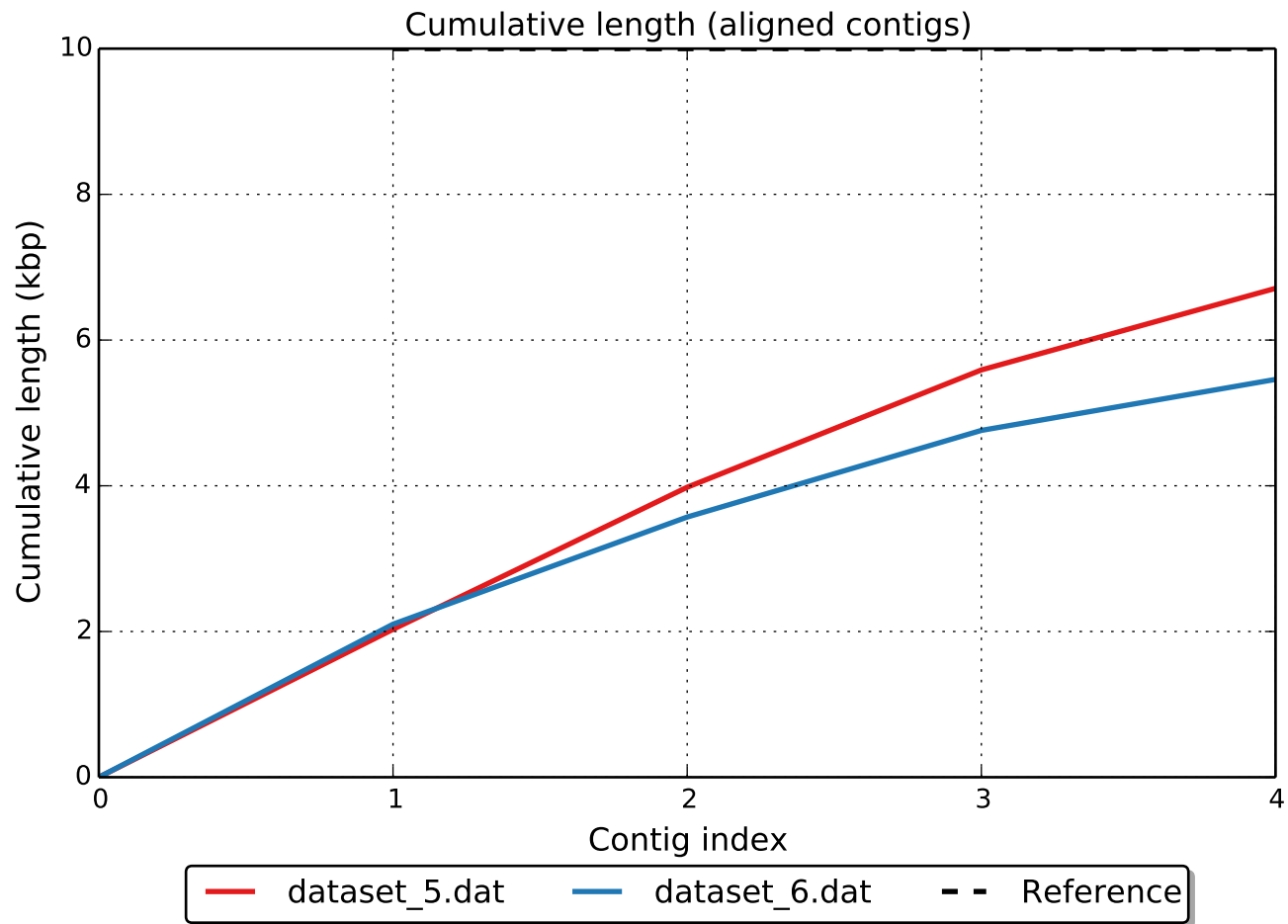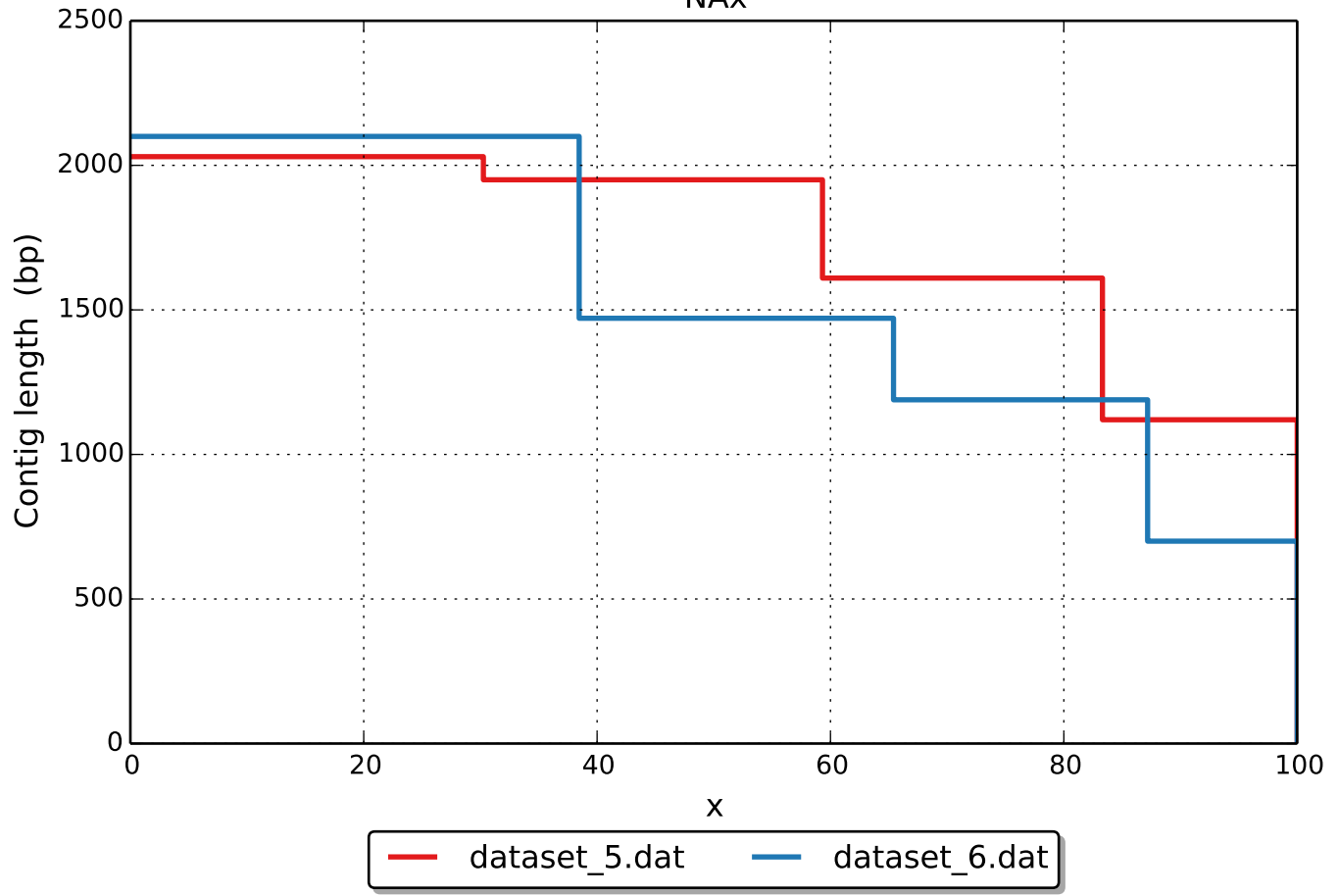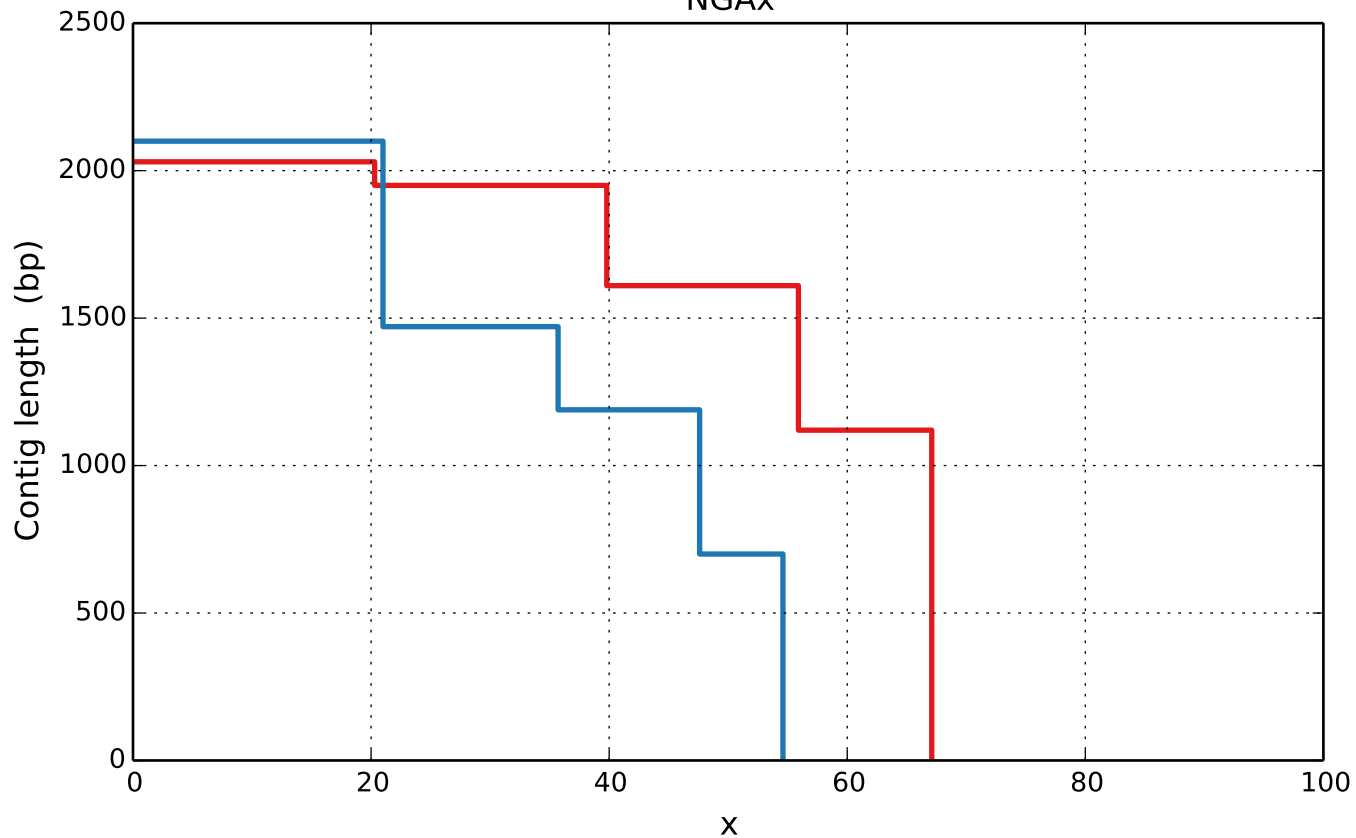(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Cumulative length

Nx

Contig length (kbp)

x

dataset_5.dat — dataset_6.dat

Misassemblies

NAx

Contig length (bp)

x

dataset_5.dat   dataset_6.dat

Cumulative # complete genes

complete genes

Cumulative # complete operons

complete operons